

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 01:34:49 ; Search time 14302.9 Seconds
(without alignments)
1528.577 Million cell updates/sec

Title: US-09-294-298-1
Perfect score: 4272
Sequence: 1 atgtctatgcccccttcag.....tggggtgctatccccatcct 4272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1118133 seqs, 2558875100 residues 2236266
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :
1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_ph.*
6: gb_pl1.*
7: gb_pl2.*
8: gb_pr1.*
9: gb_pr2.*
10: gb_pr3.*
11: em_fun.*
12: em_hum1.*
13: em_hum2.*
14: em_in.*
15: em_om.*
16: em_or.*
17: em_ov.*
18: em_pat.*
19: em_ph.*
20: em_pl.*
21: em_ro.*
22: em_sts.*
23: em_sy.*
24: em_un.*
25: em_vi.*
26: gb_hta1.*
27: gb_htg2.*
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29: gb_in2.*
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39: gb_htg7.*
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41: em_htg2.*
42: em_htg3.*
43: em_hum5.*

- 44: gb_pl3.*
- 45: gb_pr5.*
- 46: gb_htg8.*
- 47: gb_htg9.*
- 48: gb_htg10.*
- 49: gb_htg11.*
- 50: gb_htg12.*
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- 53: gb_in3.*
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- 55: gb_htg16.*
- 56: gb_htg17.*
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- 63: gb_htg19.*
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- 68: gb_pr6.*
- 69: gb_pr7.*
- 70: gb_htg20.*
- 71: gb_htg21.*
- 72: gb_htg22.*
- 73: gb_htg23.*
- 74: gb_ro.*
- 75: gb_sts1.*
- 76: gb_sts2.*
- 77: gb_sy.*
- 78: gb_un.*
- 79: gb_vil.*
- 80: gb_vil2.*
- 81: gb_pat1.*
- 82: gb_pat2.*
- 83: em_htg0.*
- 84: gb_htg24.*
- 85: gb_pr8.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	4167.4	97.6	4539	74	AF058789	Rattus no
2	4018.2	94.1	4140	74	AF058790	Rattus no
3	3940.4	92.2	4063	74	AF048976	Rattus no
4	3919	91.7	4265	74	AF050183	Rattus no
5	3602.8	84.3	4801	74	AB015962	Rattus no
6	920.8	21.6	94770	69	HSDJ570F3	Human HNA
7	920.8	21.6	150956	70	AL161903	Human HNA
8	920.8	21.6	169323	70	AL161906	Human HNA
9	627.8	14.7	4368	10	AF047711	Homo sapi
10	530	12.4	829	74	AF053938	Rattus no
11	336.4	7.9	4287	34	AK024488	Homo sat
12	241.8	5.7	56366	39	AC019800	Drosophila
13	241.8	5.7	191504	36	AC012162	Drosophila
14	241.8	5.7	202741	36	AC012161	Drosophila
15	241.8	5.7	300994	28	AB003506	Drosophila
16	236.8	5.5	3984	28	AB011280	Caenorhab
17	223.6	5.2	65961	38	AC016523	Drosophila
18	205.2	4.8	2385	34	AK022662	Homo sapi
19	196	4.6	172027	72	AL365274	Homo sapi
20	194.4	4.6	211	74	AF055883	Rattus no
21	187.6	4.4	169323	70	AL161906	Homo sapi

CHEN
1997

c 22 157 3.7 81971 68 HS593C16
23 157 3.7 156700 50 AC027051
24 139.2 3.3 155332 51 AC040900
c 25 139.2 3.3 156700 50 AC027051
26 116.4 2.7 40775 69 HS1CK721Q
c 27 116.4 2.7 200548 51 AC040962
28 113.4 2.7 4107 74 MM020238
29 103.4 2.4 159777 35 AC011703
30 103.2 2.4 157803 35 AC011492
31 100 2.3 39660 29 CEC07B5
32 99.2 2.3 2837 69 HS1NSP4BP
33 98.4 2.3 237619 56 AC073765
34 97.6 2.3 833 28 AB011285
35 95.8 2.2 2647 81 E13125
36 95.8 2.2 2730 3 BTU30857
37 93.8 2.2 760 28 AB011283
38 93.8 2.2 2276 28 AB011279
c 39 89.2 2.1 314 75 G21290
40 71.2 1.7 310 28 AB011284
c 41 70.8 1.7 5719 74 MMCAT51
c 42 70.8 1.7 180385 9 AC007461
c 43 69.6 1.6 3720 80 S76368
c 44 69.6 1.6 43658 80 HSV3PRGEN
c 45 69.6 1.6 112930 80 HSGEND

ALIGNMENTS

RESULT 1
AF058789 4539 bp mRNA ROD 14-SEP-2000
LOCUS Rattus norvegicus SynGAP-a mRNA, complete cds.
DEFINITION AF058789
ACCESSION AF058789
VERSION AF058789.2 GI:10122137
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4539)
AUTHORS Kim,J.H., Liao,D., Lau,L.F. and Haganir,R.L.
TITLE SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family
JOURNAL Neuron 20 (4), 683-691 (1998)
MEDLINE 98240917
REFERENCE 2 (bases 1 to 4539)
AUTHORS Kim,J.H. and Haganir,R.L.
TITLE Direct Submission
JOURNAL Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
COMMENT On Sep 14, 2000 this sequence version replaced gi:3065888.
FEATURES
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BASE COUNT 992 a 1448 c 1290 g 809 t
ORIGIN

Query Match 97.6% Score 4167.4; DB 74; Length 4539;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 4270; Conservative 0; Mismatches 1; Indels 82; Gaps 2;

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 Rattus.

REFERENCE 1 (bases 1 to 4140)
 Kim, J.H., Liao, D., Lau, L.F. and Haganir, R.L.
 SYNAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family
 Neuron 20 (4), 583-591 (1998)
 JOURNAL 98240917
 MEDLINE 2 (bases 1 to 4140)
 Kim, J.H. and Haganir, R.L.
 Direct Submission
 TITLE Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical
 JOURNAL Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
 REFERENCE 3 (bases 1 to 4140)
 Kim, J.H. and Haganir, R.L.
 Direct Submission
 TITLE Submitted (08-OCT-1998) Neuroscience, Johns Hopkins Medical
 JOURNAL Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
 REMARK Sequence update by submitter
 COMMENT On Oct 9, 1998 this sequence version replaced gi:3065890.
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RESULT

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LOCUS Rattus norvegicus synaptic ras GTPase-activating protein p135
DEFINITION SynGAP mRNA, complete cds.

ACCESSION AF048976
VERSION AF048976.1 GI:2935447

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 4063)

AUTHORS Chen, H.-J. and Kennedy, M.B.
TITLE Identification and cloning of a novel 130 kd protein containing a
ras GTPase-activating domain from the rat forebrain postsynaptic
density
(in) SOC. NEUROSCI. ABSTR.: 1466; (1997)

REFERENCE 2 (bases 1 to 4063)

AUTHORS Chen, H.-J., Rojas-Soto, M. and Kennedy, M.B.
TITLE A synaptic Ras GTPase-activating protein (p135 SynGAP) inhibited by
Cam kinase II
Unpublished

REFERENCE 3 (bases 1 to 4063)

AUTHORS Chen, H.-J. and Kennedy, M.B.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) Division of Biology, California Institute
of Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA
91125, USA

FEATURES

source

CDS

Seq ID
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Rattus.
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AUTHORS Suzuki,T.
TITLE SynGAP-d
JOURNAL Published Only in DataBase (1999) In press
REFERENCE 2 (bases 1 to 4801)
AUTHORS Suzuki,T.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo Suzuki, Shinshu University School of Medicine, Department of Neuroplasticity; 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan (E-mail:suzukit@sch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683, Fax:+81-263-37-2725)
COMMENT On Mar 16, 1999 this sequence version replaced gi:4239945.
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RESULT 6

HSDJ570F3/c

LOCUS

DEFINITION

HSDJ570F3 94770 bp DNA PRI 17-DEC-1999

Human DNA sequence from clone RP4-570F3 on chromosome 6. Contains a

gene similar to Rattus norvegicus synaptic ras GTPase-activating

protein p135, the C10K07210.5 (polypeptide from patented cDNA

Em: E06811) gene, the PHF1 (PHD finger protein 1) gene, the KNSL2

(kinesin-like 2) gene, the gene for acyl-protein thioesterase,

ESTs, STSs, GSSs and a CpG Island, complete sequence.

AL050332

AL050332.15 GI:6010176

HTG; C10K07210.5; CpG Island; finger protein; GTPase-activating

protein; kinesin-like; KNSL2; p135; PHD; PHF1; ribosomal protein

L12; RPL12; Syngap.

human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia: Eutheria: Primates: Catarrhini; Hominoidea: Homo.
1 (bases 1 to 94770)
Mashregni-Mohammadi, M.
Direct Submission
Submitted (17-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonequery@sanger.ac.uk
On Oct 4, 1999 this sequence version replaced gi:5870478.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.

Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA567N9
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 155424 bases at least Q40
 Consensus quality: 160003 bases at least Q30
 Consensus quality: 163252 bases at least Q20
 Insert size: 167023; sum-of-contigs
 Insert size: 186175; 5.7% error; agarose-fp
 Quality coverage: 3.59x in Q20 bases; sum-of-contigs Quality
 coverage: 3.22x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 24 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 5456: contig of 5456 bp in length
 * 5457 5556: gap of 100 bp
 * 5557 8767: contig of 3211 bp in length
 * 8768 8867: gap of 100 bp
 * 8868 17168: contig of 8301 bp in length
 * 17169 17268: gap of 100 bp
 * 17269 26591: contig of 9323 bp in length
 * 26592 26691: gap of 100 bp
 * 26692 31188: contig of 4497 bp in length
 * 31189 31288: gap of 100 bp
 * 31289 37579: contig of 6291 bp in length
 * 37580 37679: gap of 100 bp
 * 37680 45350: contig of 7671 bp in length
 * 45351 45450: gap of 100 bp
 * 45451 48354: contig of 2904 bp in length
 * 48355 48454: gap of 100 bp
 * 48455 63401: contig of 14947 bp in length
 * 63402 63501: gap of 100 bp
 * 63502 67724: contig of 4223 bp in length
 * 67725 67824: gap of 100 bp
 * 67825 70550: contig of 2726 bp in length
 * 70551 70650: gap of 100 bp
 * 70651 80664: contig of 10014 bp in length
 * 80665 80764: gap of 100 bp
 * 80765 83307: contig of 2543 bp in length
 * 83308 83407: gap of 100 bp
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 * 88384 88483: gap of 100 bp
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 * 99355 99454: gap of 100 bp
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 * 111056 111153: gap of 100 bp
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 * 138060 151691: contig of 13632 bp in length
 * 151692 151791: gap of 100 bp
 * 151792 158253: contig of 6462 bp in length
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 829)
 AUTHORS Chen,H.-J. and Kennedy,M.B.
 TITLE Identification and cloning of a novel 130 kd protein containing a
 ras GTPase-activating domain from the rat forebrain postsynaptic
 density
 JOURNAL Abstr. - Soc. Neurosci. 23, 1466-1466 (1997)
 REFERENCE 2 (bases 1 to 829)
 AUTHORS Chen,H.-J., Rojas-Soto,M., Oguni,A. and Kennedy,M.B.
 TITLE A synaptic Ras-GTPase activating protein (pl35 SynGAP) inhibited by
 Cam kinase II
 JOURNAL Neuron 20 (5), 895-904 (1998)
 MEDLINE 98282016
 REFERENCE 3 (bases 1 to 829)
 AUTHORS Chen,H.-J. and Kennedy,M.B.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-1998) Biology, California Institute of
 Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA.

FEATURES	source
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 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 191504)
 Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Gallie, R., George, R.A., Harris, N.L.,
 Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
 Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R.,
 Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B.,
 Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,
 Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
 Sequencing of Drosophila melanogaster
 Unpublished
 REFERENCE
 2 (bases 1 to 191504)
 Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Farfan, D.E., Gallie, R., George, R.A., Harris, N.L.,
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 Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
 Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
 Rubin, G.M.

Direct Submission

Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Feb 11, 2000 this sequence version replaced gi:6838925.

For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases.

* NOTE: this is a 'working draft' sequence. It currently

* consists of 142 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 456: contig of 456 bp in length
 * 457 536: gap of unknown length
 * 537 1004: contig of 468 bp in length
 * 1005 1084: gap of unknown length
 * 1085 1958: contig of 874 bp in length
 * 1959 2038: gap of unknown length
 * 2039 2248: contig of 210 bp in length
 * 2249 2328: gap of unknown length
 * 2329 2858: contig of 530 bp in length
 * 2859 2938: gap of unknown length
 * 2939 3325: contig of 387 bp in length
 * 3326 3405: gap of unknown length
 * 3406 4165: contig of 760 bp in length
 * 4166 4245: gap of unknown length
 * 4246 4716: contig of 471 bp in length
 * 4717 4796: gap of unknown length
 * 4797 5373: contig of 577 bp in length
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 * 5454 6051: contig of 597 bp in length
 * 6051 6130: gap of unknown length
 * 6131 6720: contig of 590 bp in length
 * 6721 6800: gap of unknown length
 * 6801 7461: contig of 661 bp in length
 * 7462 7541: gap of unknown length
 * 7542 8104: contig of 563 bp in length
 * 8105 8184: gap of unknown length
 * 8185 8505: contig of 321 bp in length
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 * 8586 9227: contig of 642 bp in length
 * 9228 9307: gap of unknown length
 * 9308 10091: contig of 784 bp in length
 * 10092 10171: gap of unknown length
 * 10172 11099: contig of 928 bp in length
 * 11100 11179: gap of unknown length
 * 11180 11747: contig of 568 bp in length
 * 11748 11827: gap of unknown length
 * 11828 12768: contig of 940 bp in length
 * 12769 12847: gap of unknown length
 * 12848 13398: contig of 551 bp in length
 * 13399 13478: gap of unknown length
 * 13479 14007: contig of 529 bp in length
 * 14008 14087: gap of unknown length
 * 14088 14867: contig of 780 bp in length
 * 14868 14947: gap of unknown length
 * 14948 15562: contig of 615 bp in length
 * 15563 15642: gap of unknown length
 * 15643 16859: contig of 1217 bp in length
 * 16860 16933: gap of unknown length

TITLE
JOURNAL

COMMENT

* 16940 17986: contig of 1047 bp in length
* 17987 18066: gap of unknown length
* 18067 19341: contig of 1275 bp in length
* 19342 19421: gap of unknown length
* 19422 20926: contig of 1505 bp in length
* 20927 21006: gap of unknown length
* 21007 21533: contig of 1147 bp in length
* 21534 22233: gap of unknown length
* 22234 23236: contig of 1003 bp in length
* 23237 23316: gap of unknown length
* 23317 24607: contig of 1291 bp in length
* 24608 24687: gap of unknown length
* 24688 25620: contig of 933 bp in length
* 25621 25700: gap of unknown length
* 25701 26300: contig of 600 bp in length
* 26301 26380: gap of unknown length
* 26381 27488: contig of 1108 bp in length
* 27489 27568: gap of unknown length
* 27569 28215: contig of 647 bp in length
* 28216 28295: gap of unknown length
* 28296 29440: contig of 1145 bp in length
* 29441 29520: gap of unknown length
* 29521 30587: contig of 1067 bp in length
* 30588 30667: gap of unknown length
* 30668 32042: contig of 1375 bp in length
* 32043 32122: gap of unknown length
* 32123 37400: contig of 1618 bp in length
* 37401 37480: gap of unknown length
* 37481 38211: contig of 1555 bp in length
* 38212 38455: gap of unknown length
* 38456 38528: contig of 803 bp in length
* 38529 38638: gap of unknown length
* 38639 38803: gap of unknown length
* 38804 38909: contig of 1426 bp in length
* 38910 39589: gap of unknown length
* 39590 40719: contig of 1130 bp in length
* 40720 40799: gap of unknown length
* 40800 42453: contig of 1654 bp in length
* 42454 42533: gap of unknown length
* 42534 43841: contig of 1308 bp in length
* 43842 43921: gap of unknown length
* 43922 44100: contig of 1489 bp in length
* 44111 44900: gap of unknown length
* 44901 46782: contig of 1292 bp in length
* 46783 46862: gap of unknown length
* 46863 48570: contig of 1708 bp in length
* 48571 48650: gap of unknown length
* 48651 51042: contig of 2392 bp in length
* 51043 51122: gap of unknown length
* 51123 52760: contig of 1638 bp in length
* 52761 52840: gap of unknown length
* 52841 54712: contig of 1872 bp in length
* 54713 54792: gap of unknown length
* 54793 56521: contig of 1729 bp in length
* 56522 56601: gap of unknown length
* 56602 58938: contig of 2337 bp in length
* 58939 59018: gap of unknown length
* 59019 60837: contig of 1819 bp in length
* 60838 60917: gap of unknown length
* 60918 62986: contig of 2071 bp in length
* 62989 63068: gap of unknown length
* 63069 65583: contig of 2515 bp in length
* 65584 65663: gap of unknown length
* 65664 68774: contig of 3111 bp in length
* 68775 68854: gap of unknown length
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* 71236 71315: gap of unknown length
* 71316 74113: contig of 2798 bp in length
* 74114 74193: gap of unknown length
* 74194 77405: contig of 3212 bp in length
* 77406 77486 80936: contig of 3451 bp in length

* 80937 81016: gap of unknown length
* 81017 83357: contig of 2341 bp in length
* 83358 83437: gap of unknown length
* 83438 87456: contig of 4019 bp in length
* 87457 87536: gap of unknown length
* 87537 91532: contig of 3996 bp in length
* 91533 91612: gap of unknown length
* 91613 97143: contig of 5531 bp in length
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* 97224 105593: contig of 8370 bp in length
* 105594 105673: gap of unknown length
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* 112072 112151: gap of unknown length
* 112152 121011: contig of 8860 bp in length
* 121012 121091: gap of unknown length
* 121092 143113: contig of 22022 bp in length
* 143114 143193: gap of unknown length
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* 143928 144007: gap of unknown length
* 144008 144842: contig of 835 bp in length
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* 144923 145360: contig of 438 bp in length
* 145361 145440: gap of unknown length
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Db 113379 GAGCGGACCTTTGGATCTACTCGTCGCAAGTCGATCGCTCCGAATGCGAGACACG 113381
QY 727 cgcgggttagaactgtgaaactatgataagctcgaagctcgaagctcgcaccccaag 760
Db 113439 CGTCCGACGACAACTCGCTGAAGATGTTGGTGTACGAGCGGGAANAATCTTCGCCCAAG 113498
QY 787 aagcgtatctactgcgagttatgcctggagacacatgctctatgcacgacacacttccaa 846
Db 113499 AAGCGTTACTTTTGGCAACTGCAATTTGGACAAGACGCTGACGCGCGGAGATTCGGTGAAG 113558
QY 847 ccccgctcagctcaggagacactgtcttttggggcgagcacttcgagtttaacaacctg 906
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QY 1087 ggcctgggggaggggggtcagggggtcagggggtcagggggaagggagggcgtg 1146
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QY 1147 cctgctgtcggctgaagcccggttacacagacaatagatcctgcccagagctatat 1206
Db 113832 CCCACGCTGAGGATCAAGTGTGTTTCCAGAGACACCCGACATCTCTCCCAATGTGTAC 113891
QY 1207 aaggagtttcagaatatgtgaccaaacactacccgcatcgtctgtgctgctggagccc 1266
Db 113892 GGCAACTTTTTCACGTACCTCAAGGAGAACTATTAAGCGCGTGTGCGAGACCTTGGAGCG 113951

* 14607 15801: contig of 1195 bp in length
 * 15802 13881: gap of unknown length
 * 15882 16640: contig of 759 bp in length
 * 16641 16720: gap of unknown length
 * 16721 17679: contig of 959 bp in length
 * 17680 17759: gap of unknown length
 * 17760 18797: contig of 1038 bp in length
 * 18798 18877: gap of unknown length
 * 18878 19555: contig of 1078 bp in length
 * 19556 20035: gap of unknown length
 * 20036 20931: contig of 896 bp in length
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 * 21012 21643: contig of 632 bp in length
 * 21644 21723: gap of unknown length
 * 21724 23416: contig of 1693 bp in length
 * 23417 23496: gap of unknown length
 * 23497 24457: contig of 961 bp in length
 * 24458 24537: gap of unknown length
 * 24538 25955: contig of 1418 bp in length
 * 25956 26035: gap of unknown length
 * 26036 27838: contig of 1803 bp in length
 * 27839 27918: gap of unknown length
 * 27919 29886: contig of 1768 bp in length
 * 29887 29766: gap of unknown length
 * 29767 30976: contig of 1210 bp in length
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 * 32461 32540: gap of unknown length
 * 32541 34644: contig of 2104 bp in length
 * 34645 34724: gap of unknown length
 * 34725 36341: contig of 1617 bp in length
 * 36342 37864: contig of 1443 bp in length
 * 37865 37944: gap of unknown length
 * 37945 39424: contig of 1480 bp in length
 * 39425 39504: gap of unknown length
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 * 41342 41421: gap of unknown length
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 * 44420 44499: gap of unknown length
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 * 82126 85135: contig of 3010 bp in length
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 * 85216 88550: contig of 3335 bp in length

* 88551 88630: gap of unknown length
 * 88631 92611: contig of 3981 bp in length
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 * 154740 154819: gap of unknown length
 * 154820 155338: contig of 519 bp in length
 * 155339 155418: gap of unknown length
 * 155419 155993: contig of 575 bp in length
 * 155994 156073: gap of unknown length
 * 156074 156806: contig of 733 bp in length
 * 156807 156886: gap of unknown length
 * 156887 157541: contig of 655 bp in length
 * 157542 157621: gap of unknown length
 * 157622 158208: contig of 587 bp in length
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Query Match 5.7%; Score 241.8; DB 36; Length 202741;
 Best Local Similarity 50.6%; Pred. No. 3.2e-37;
 Matches 749; Conservative 0; Mismatches 682; Indels 48; Gaps 5;

QY 667 gaaaggacaaatgagatgagaatctacagagggtgtgaaacccaagacacacagc 726
 DB 126449 GAGCGGACCTTTGGGATCTACTCGCTGGCAAGTGGTCCGTAATGCGAGACACG 126390
 QY 727 cgcgggtagataaagctgctgaactatgagatcagaagctcgagagctcccccccaag 786
 DB 126389 CGTCGACGACACACTCGCTGAAGATGGGGGTAGCGGCGGAGAAATCTGCGCCCAAG 126330
 QY 787 aagcgatatactgaggttatgctgtgacgacatgctctatgacgacgacactccaag 841
 DB 126329 AAGCGTTACTTTGGCAACTGCAATTTGGACAAGACGCTGTACGCGCGGACTTCGTGAAG 126270
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 Db 125099 CTACACAGTTTGTCTACGGAAGCCCTGGCCAACTCCCGGAGGCGCAGGACGAGCTG 125040

Qy 2089 ggcgcgtgccccgctctctcagcgcacatcagcacagcc 2127
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 VERSION AE003506.1 GI:7293355
 KEYWORDS HTG.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 AUTHORS Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Ananides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blaziej,B.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,A., Baxter,E.G., Helt,G., Nelson,C.R., Gabor Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J., Andrews-Fiankoch,C., Baldwin,D., Ballew,R.M., Beeson,K.Y., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Bertram,B.P., Bhattacharya,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brottier,P., Burtis,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferreira,S., Fleischmann,W., Flosser,C., Gabriellian,A.E., Garg,N.S., Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Iqbal,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.N., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusskern,D.R., Pacleib,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Swirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.

TITLE The genome sequence of Drosophila melanogaster
 JOURNAL Science 287 (5461), 2185-2195 (2000)
 MEDLINE 20196006
 REFERENCE 2 (bases 1 to 300994)
 AUTHORS Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,J.C.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
3177.191 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 10
1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95.8	2.2	2647	18 T76739	CDNA encoding active type R-Ras protein binding protein p98.
2	63.6	1.5	1337	20 Z17263	Human gene express
3	61	1.4	795	19 V55830	FlcA insert stabl
4	61	1.4	799	19 V55831	Nucleotide sequenc
5	61	1.4	5452	20 X30923	Anti-sense strand
6	61	1.4	8705	20 Z23778	Vector pShuttle DN
7	61	1.4	9600	19 V21683	Vector plasmid pCM
8	61	1.4	10380	20 Z22248	Nucleotide sequenc
9	61	1.4	10596	14 Q51731	Plasmid pcISEBON f
10	61	1.4	10596	17 T40348	Plasmid pcISEBON f
11	61	1.4	10596	20 X15650	Nucleotide sequenc
12	59.6	1.4	1925	20 X90924	Epstein Barr Virus

13	59.4	1.4	1908	8 N71064	Gene encoding plas
14	59.2	1.4	1000	21 A02484	Human colon cancer
15	57.8	1.4	49999	20 Z23895	Murine l080 homolo
16	57.6	1.3	2338	19 V23249	Nephila clavipes s
17	57.6	1.3	2338	21 Z38195	N. clavipes spider
18	56	1.3	2000	8 N71065	Gene encoding plas
19	56	1.3	2338	12 Q14183	N.clavipes draglin
20	56	1.3	16442	18 X83006	Partial mouse WRN
21	55.8	1.3	2004	18 T85356	Nephila clavipes s
22	54.6	1.3	32207	20 V73805	KSHV LUR DNA (nucl
23	54.6	1.3	137507	19 V19941	KSHV long unique c
24	54.4	1.3	9551	20 Z23301	cDNA encoding a hu
25	54	1.3	543	13 Q23092	Antigen tc-7a gene
26	53.6	1.3	1995	12 Q14184	N.clavipes draglin
27	53.6	1.3	1995	19 V23250	Nephila clavipes s
28	53.6	1.3	1995	21 Z38196	N. clavipes spider
29	53.4	1.2	4055	20 Z40484	Human ZC2 DNA. Ho
30	53.4	1.2	4180	21 A10669	Human protein kina
31	53	1.2	1137	14 Q33061	Plasmodium vivax c
32	52.6	1.2	10732	21 A10594	Gene encoding a su
33	52.4	1.2	114955	20 X53491	Human adenosine A1
34	52.2	1.2	1847	19 V04694	Cell cycle protein
35	51.4	1.2	3198	20 X02974	Human IL-1ra BAC c
36	51.2	1.2	2744	16 Q98470	Mispl-containing p
37	51.2	1.2	51259	18 X83007	Partial mouse WRN
38	50.2	1.2	1886	16 Q87587	DNA encoding Leuco
39	49	1.1	2040	18 T62137	Leishmania brazili
40	49	1.1	2040	19 V47557	Leishmania antigen
41	48.8	1.1	1218	21 A02488	Human colon cancer
42	48.8	1.1	2313	20 Z07197	Human lung tumour
43	48.6	1.1	1432	19 V47585	Leishmania antigen
44	47.8	1.1	3337	17 T34620	P. vivax ESP-1 blo
45	47.8	1.1	3337	20 X15174	DNA encoding a sec

ALIGNMENTS

RESULT 1
T76739
ID T76739 standard; cDNA; 2647 BP.
XX
AC T76739;
XX
DT 08-OCT-1997 (first entry)
XX
DE cDNA encoding active type R-Ras protein binding protein p98.
XX
KW Active-type-R-Ras protein; p98; tumour; disease; cancer;
KW cellular Ca ion; phospholipid; tumour forming promoter;
KW tumour forming inhibitor; ss.
XX
OS Bos taurus.
XX
FH Key
CDS 13..2517
FT /*tag= a
FT /product= p98
XX
XX JP09135688-A.
PN
XX
PD 27-MAY-1997.
XX
PF 16-NOV-1995; 95JP-0298720.
XX
PR 16-NOV-1995; 95JP-0298720.
XX
PA (KIRI) KIRIN BREWERY KK.
XX
XX WPI; 1997-335993/31.
DR P-PSDB; W24227.
XX
PT Active R-Ras protein-binding protein p98 - used in the treatment of

PT	cancer, and diseases related to cellular calcium ion concentrations
XX	
PS	Claim 9; Page 9-12; 18pp; Japanese.
XX	
CC	This sequence encodes a protein capable of binding to active-type-R-Ras
CC	protein. The protein has a molecular weight of 98 kD by SDS-PAGE, and
CC	is designated p98. The protein coding sequence can be inserted into a
CC	suitable vector to treat certain tumours or diseases (various cancers)
CC	in which active R-Ras protein is involved. Because active R-Ras protein
CC	is involved in formation and inhibition of tumours and related to
CC	diseases in which cellular Ca ions or phospholipids are involved, the
CC	screening method can be used for screening e.g. a tumour forming promoter
CC	or tumour forming inhibitor.
XX	
SQ	Sequence 2647 BP; 633 A; 764 C; 769 G; 481 T; 0 other;

Query Match	2.2%;	Score 95.8;	DB 18;	Length 2647;
Best Local Similarity	50.9%;	Pred. No. 1.7e-12;		
Matches 310;	Conservative	0;	Mismatches 287;	Indels 12;
				Gaps 3

QY	1278	caaggcgaaggagaggtcgtctagtgcaactggttcacatcctgcgaagcacagcgcaaggc	1337
Db	996	caggggagaagcagagggcgccatcccgctggtcgcgctctctctgcatctacggccgggt	1055
QY	1338	caaggacttccttcagacatggccatgtccagagtagacgggttcattgagcggggaaca	1397
Db	1056	ggtgccttcacagcgccatcgccagcgcgaggctcgaggaaccagagacc---ccaa	1112
QY	1398	cctcatattccggagaaacacgctgcgcactaaagccataagaagtagtatagactgat	1457
Db	1113	taagatcttcagggaactcgctgacatccaagtgcctcgatgagcagatgaagctggc	1172
QY	1458	tggccaagaataacctcaagatggccattggggaggttcattccgggctctgtatgaattcga	1517
Db	1173	agsgatgcagtactacagtcacccctgaacccaccatagagagatttgcagagtca	1232
QY	1518	ggagaactgtgaagttagaccccatcaagtgcacagcgtcc---agctctggcagagacca	1574
Db	1233	taagtctgtgaattgaccccgtaggctgaaggacggcgagagcctagagagacaacat	1292
QY	1575	ggccaacctgcggatgtgctgtgagttggccctgtgcaggttgatccactcccatctcgt	1634
Db	1293	ggagaacctgcggcagttgttgaccgctgttcacgctcatcaccaaaatcggggtcgag	1352
QY	1635	gttcccgaggagcgtgaaggaaggttttgcatcatgtgcgctgcgctgtgcagagcgggg	1694
Db	1353	ctgccccaacgtcatgtgtgacatcttctccctcgggagcagcgccaaagcgtt	1412
QY	1695	ccgggagagacattcgtg-----acaggctgatcagcgctcgctctctctcgcttctt	1748
Db	1413	ccaggatgacctggacgtgcggtgtacacagctgtgagcagcttcatttctcgcggttctt	1472
QY	1749	ctgcccgccatcatgtcgcaccagtcgttttggactgatgcaggagtagccacagatgacca	1808
Db	1473	cgctccagccatctctgcccccaacctcttccagctcagccccaccacacgagccaccaca	1532
QY	1809	gacctcaagaacctcaacctcatgcgaaggttatccagaacctggccaaacttttccaa	1868
Db	1533	gaactcgaagacgtcaactgttttccaadaccattcagactctggcagcctgtgccaa	1592

RESULT	2
Z17263	
ID	Z17263 standard; cDNA; 1337 BP.
XX	
AC	Z17263;
XX	
DT	12-OCT-1999 (first entry)

XX	Human gene expression product	cdNA sequence	SEQ ID NO:4735.
DE	Human; gene;	gene expression product;	diagnosis; therapy; probe;
XX	KW	detection; mapping;	tissue typing; profiling; forensic; cancer;
KW	KW	genetic analysis;	colorectal cancer; breast cancer; lung cancer;
XX	OS	Homo sapiens.	
OS	XX		
XX	PN	WO938972-A2.	
XX	PN		
XX	PD	05-AUG-1999.	
XX	XX		
XX	XX	28-JAN-1999;	99WO-US01619.
XX	XX		
XX	XX	03-APR-1998;	98US-0080666.
PR	PR	28-JAN-1998;	98US-0072910.
XX	XX	24-FEB-1998;	98US-0075954.
PR	PR	31-MAR-1998;	98US-0080114.
XX	XX	03-APR-1998;	98US-0080515.
XX	XX		
XX	XX	{CHIR } CHIRON CORP.	
XX	XX	{HYSE-} HYSEQ INC.	
XX	XX		
XX	XX	Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;	
PI	PI	Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;	
PI	PI	Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;	
PI	PI	Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;	
PI	PI	Stache-Crain B, Sudduth-Klinger J, Williams LT;	
XX	XX		
XX	XX	WPI; 1999-494092/41.	
XX	XX		
XX	XX	Novel human genes and their expression products which are	
PT	PT	differentially expressed in different cell types	
PT	PT		
XX	XX		
PS	PS	Claim 1; Page 2250-2251; 2479pp; English.	

The present invention describes a library of human polynucleotides comprising the sequences given in 12532 to 17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in 12532 to 17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.

SQ Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
 Query Match 1.5%; Score 63.6; DB 20; Length 1337;
 Best Local Similarity 33.0%; Pred. No. 2.7e-05;
 Matches 147; Conservative 0; Mismatches 298; Indels 0; Gaps 0;

[illegible]

Best 11.3%

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 01:35:57 ; Search time 6516.34 Seconds
(without alignments)
4593.988 Million cell updates/sec

Title: US-09-294-298-1
Perfect score: 4272
Sequence: 1 atgtctatgcccccttcag.....tggggtctatccccctct 4272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues 15983484
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: gb_est3: *
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7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *
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13: gb_est13: *
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 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	490.4	11.5	571	37	AV590698	AV590698 AV590698
2	383.8	9.0	474	181	A2399131	A2399131 LM0164P14
3	294.6	6.9	593	95	AW779747	AW779747 hn85f10.x
4	250.4	5.9	463	108	BE463433	BE463433 hw23d06.x
5	244.6	5.7	427	11	AA709010	AA709010 zf94h11.s
6	233.6	5.5	597	90	AW421227	AW421227 fj94f10.x
7	228.8	5.4	682	173	AQ993964	AQ993964 RPCI-23-2
8	228.8	5.2	566	22	AI606711	AI606711 ml58d01.y
9	221.8	5.2	413	10	AA691827	AA691827 vt05d01.y
10	214	5.0	707	28	AJ396547	AJ396547 AJ396547
11	211.8	5.0	555	27	AI958829	AI958829 fd22d01.y
12	201	4.7	628	108	BE490923	BE490923 db38g08.x
13	197.2	4.6	516	111	BE695645	BE695645 MRI-BT080
14	195.8	4.6	347	87	AW204612	AW204612 UI-H-B11
15	195.4	4.6	596	136	BE848541	BE848541 uw39f05.y
16	190	4.4	481	135	BE773015	BE773015 RCI-FR013
17	185	4.3	542	93	AW656799	AW656799 109245 MA
18	182.2	4.3	296	23	AI650331	AI650331 wa18f01.x
19	177.6	4.2	345	39	AW076911	AW076911 fj03d08.y
20	173	4.0	511	22	AI577567	AI577567 UI-R-YO-y
21	167.2	3.9	388	183	BE68208	BE68208 C1978SK-A-
22	165.6	3.9	474	87	AW205989	AW205989 UI-H-B11-
23	161.2	3.8	460	22	AI609604	AI609604 tw91e09.x
24	157.8	3.7	1020	191	CNS02YGV	AI215753 Tetraodon
25	157	3.7	449	9	AA554056	AA554056 n101q07.s
26	154.6	3.6	440	2	AA107246	AA107246 ml58d01.r
27	149.4	3.5	651	19	AI327335	AI327335 mp74c11.x
28	148.6	3.5	877	192	CNS04DL0	AI285885 Tetraodon
29	146.8	3.4	443	40	AW136165	AW136165 UI-H-B11-
30	146.8	3.4	464	95	AW826497	AW826497 fk62h05.x
31	146	3.4	452	9	AA554055	AA554055 n101q06.s
32	145.4	3.4	407	133	BE015978	BE015978 fk62h05.y
33	139.8	3.3	382	22	AI562171	AI562171 vw73f04.x
34	138.6	3.2	317	91	AW527364	AW527364 UI-R-B01-
35	138.6	3.2	457	2	AA118397	AA118397 mp74c11.r
36	138.4	3.2	268	92	AW593427	AW593427 hg15e10.x
37	136.6	3.2	379	9	AA575948	AA575948 nm56d05.s
38	135.6	3.2	554	111	BE723198	BE723198 192621 MA
39	133.4	3.1	336	26	AI874961	AI874961 ul27f03.x
40	131.8	3.1	694	28	AJ399084	AJ399084 AJ399084
41	130.4	3.1	335	134	BE085114	BE085114 CM2-BT066
42	130	3.0	1006	190	CNS00HWF	AI073826 Drosophil
43	128.2	3.0	631	191	CNS01X05	AI172022 Tetraodon
44	126.8	3.0	975	191	CNS03ANH	AI235430 Tetraodon
45	124.2	2.9	397	111	BE695651	BE695651 MRI-BT080

ALIGNMENTS

RESULT 1
 AV590698
 LOCUS AV590698 571 bp mRNA
 DEFINITION AV590698 Bos taurus brain fetus Bos taurus cDNA clone ElBR014B04
 5', mRNA sequence.
 ACCESSION AV590698
 VERSION AV590698.1 GI:9701691
 KEYWORDS EST.
 SOURCE COW.

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 01:40:05 ; Search time 231 Seconds
(without alignments)
2980.419 Million cell updates/sec

Title: US-09-294-298-1
Perfect score: 4272
Sequence: 1 atgtcctatgcccccttcag,.....tggggtgctatcccatcct 4272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PTCYS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	63.6	1.5	3148	3	US-08-909-954-1	Sequence 1, Appl
2	63.4	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
3	62	1.5	3117	3	US-08-909-954-3	Sequence 3, Appl
4	61	1.4	2580	3	US-09-050-863-2	Sequence 2, Appl
5	61	1.4	5452	2	US-09-130-114-1	Sequence 1, Appl
6	61	1.4	10596	1	US-07-884-811-15	Sequence 15, Appl
7	61	1.4	10596	1	US-07-885-971-15	Sequence 15, Appl
8	61	1.4	10596	1	US-08-087-783A-15	Sequence 15, Appl
9	61	1.4	10596	1	US-08-194-088B-15	Sequence 15, Appl
10	61	1.4	10596	2	US-08-194-087-15	Sequence 15, Appl
11	61	1.4	10596	4	PCR-US93-0464B-15	Sequence 15, Appl
12	57.6	1.3	2338	1	US-08-425-069-1	Sequence 1, Appl
13	57.6	1.3	2338	2	US-08-317-844B-1	Sequence 1, Appl
14	56	1.3	16442	3	US-08-781-891-208	Sequence 1, Appl
15	54.6	1.3	3489	2	US-08-728-323B-1	Sequence 1, Appl
16	54.6	1.3	32207	2	US-08-770-379-20	Sequence 20, Appl
17	54.4	1.3	9551	1	US-08-056-200-93	Sequence 93, Appl
18	54.4	1.3	9551	2	US-08-800-644-93	Sequence 93, Appl
19	54	1.3	543	5	5273301-6	Patent No. 5273301
20	53.6	1.3	1995	1	US-08-425-069-3	Sequence 3, Appl
21	53.6	1.3	1995	2	US-08-317-844B-3	Sequence 3, Appl
22	53	1.2	1137	5	5171843-8	Patent No. 5171843
23	52.2	1.2	1847	3	US-08-675-885-4	Sequence 4, Appl
24	51.4	1.2	697	5	5171843-10	Patent No. 5171843
25	51.4	1.2	152331	3	US-09-128-155-16	Sequence 16, Appl
26	51.2	1.2	2793	1	US-08-209-747-1	Sequence 1, Appl
27	51.2	1.2	2793	3	US-08-458-298-1	Sequence 1, Appl
28	51.2	1.2	51259	3	US-08-781-891-209	Sequence 209, Appl

RESULT

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US-08-909-954-1
; Sequence 1, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: GAP12 Genes and their Uses
; FILE REFERENCE: SEQ-11P
; CURRENT APPLICATION NUMBER: US/08/909,954A
; CURRENT FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3148
; TYPE: DNA
; ORGANISM: H. sapiens
US-08-909-954-1

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ALIGNMENTS

29	49	1.1	2040	2	US-08-533-669A-5	Sequence 5, Appli
30	47.8	1.1	3337	1	US-08-072-610-1	Sequence 1, Appli
31	47.8	1.1	3337	1	US-08-719-822B-1	Sequence 1, Appli
32	47.6	1.1	337	3	US-09-253-691-3	Sequence 3, Appli
33	46	1.1	234	1	US-08-469-802B-3	Sequence 3, Appli
34	46	1.1	234	2	US-08-267-803B-3	Sequence 3, Appli
35	46	1.1	2818	1	US-08-366-276-1	Sequence 1, Appli
36	46	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
37	45	1.1	3456	1	US-08-190-687B-24	Sequence 7, Appli
38	45	1.0	4437	2	US-08-804-237C-7	Sequence 7, Appli
39	44.8	1.0	44377	2	US-08-804-198-1	Sequence 1, Appli
40	44.8	1.0	44377	2	US-08-804-198-1	Sequence 1, Appli
41	44.6	1.0	533	5	5462709-5	Patent No. 5462709
42	44.4	1.0	1599	3	US-08-853-733B-1	Sequence 1, Appli
43	44.4	1.0	1603	3	US-08-675-885-6	Sequence 6, Appli
44	44.4	1.0	1931	2	US-09-130-114-2	Sequence 2, Appli
45	43.8	1.0	2385	1	US-08-393-333-1	Sequence 1, Appli

RESULT 1

US-08-909-954-1

Sequence 1, Application US/08090954A

Patent No. 6100058

GENERAL INFORMATION:

APPLICANT: Allen, Maxine J.

APPLICANT: Buckler, Alan J.

TITLE OF INVENTION: GAP12 Genes and their Uses

FILE REFERENCE: SEQ-11P

CURRENT APPLICATION NUMBER: US/08/909,954A

CURRENT FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3148

TYPE: DNA

ORGANISM: H. sapiens

US-08-909-954-1

Query Match 1.5%; Score 63.6; DB 3; Length 3148;

Best Local Similarity 50.0%; Pred. No. 5.3e-06;

Matches 159; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY	1552	gcgtccagctcggcagagcaccaggccacactcgcggatgtcgtgtgagttgtgcccctgtgc	1611
Db	1518	gagaccagctgggctgctgacggctacactcgggccatcgtggagccatcgtgggc	1577
QY	1612	aagtgatcaactcccatcgtgtttcccgaggagactgaagagagtgattgttcacatcg	1671
Db	1578	tcctggggcgctgccgcgcgcacatcgccctcctcaacagactcaccgcgcagtg	1637
QY	1672	cggctgcgtgtgcagagcggggcccgaggacatctgtgacagctgatcagcgcctcg	1731
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QY	1732	ctctctcgcgtcttcctcgtcccgcccatcatgtgcccagctctgtttggactgatgcag	1791
Db	1698	ctctcttgcgattcttcgcacctgccttaccaccaagcttcttgaccttcggagac	1757
QY	1792	gagtaaccagatgagcagacactcagcaacccctaccctcatcgcgcaaggattatccagaac	1851
Db	1758	caaacgcggacccccccagctagcgtcactgctgtgttctgcgcaaggctgcagagc	1817
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Db	1818	attgaaacctggqccag	1835

RESULT 2
US-08-232-463-14/c

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenLin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTgpt-FJ5
; US-08-232-463-14

Query Match 1.5%; Score 63.4; DB 1; Length 7218;
Best Local Similarity 3.3%; Pred. No. 8.3e-06;
Matches 13; Conservative 233; Mismatches 149; Indels 0; Gaps 0;

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Db 1436 ACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1377
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Db 1376 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1317
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QY 3635 asagacagaccagaatctgatgcagtcacaagcccgcctgagcagagcgaagc 3694
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Db 1256 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1197
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